# PROFILING OF PROTEASE SPECIFICITY USING COMBINATORIAL FLUOROGENIC SUBSTRATE LIBRARIES


## ABSTRACT OF THE DISCLOSURE

A method is presented for the preparation and use of fluorogenic peptide substrates that allows for the configuration of general substrate libraries to rapidly identify the primary and extended specificity of enzymes, such as proteases. The substrates contain a fluorogenic-leaving group, such as 7-amino-4-carbamoylmethyl-coumarin (ACC). Substrates incorporating the ACC leaving group show comparable kinetic profiles as those with the traditionally used 7-amino-4-methyl-coumarin (AMC) leaving group. The bifunctional nature of ACC allows for the efficient production of single substrates and substrate libraries using solid-phase synthesis techniques. The approximately 3-fold increased quantum yield of ACC over AMC permits reduction in enzyme and substrate concentrations. As a consequence, a greater number of substrates can be tolerated in a single assay, thus enabling an increase in the diversity space of the library. Soluble positional protease substrate libraries of 137,180 and 6,859 members, possessing amino acid diversity at the P4-P3-P2-P1 and P4-P3-P2 positions, respectively, were constructed. Employing this screening method the substrate specificities of a diverse array of proteases were profiled, including the serine proteases thrombin, plasmin, factor Xa, uPA, tPA, granzyme B, trypsin, chymotrypsin, human neutrophil elastase, and the cysteine proteases papain and cruzain. The resulting profiles create a pharmacophoric portrayal of the proteases allowing for the design of selective substrates and potent inhibitors.